



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/659,326  
Source: OIP  
Date Processed by STIC: 9-22-03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 10/659, 326

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ Wrapped Nucleics  
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☒ Use of <220> Sequence(s) 1-20 missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/659,326

DATE: 09/22/2003

TIME: 13:13:53

Input Set : A:\NANJ-0009-1 Sequence Listing.asc

Output Set: N:\CRF4\09222003\J659326.raw

3 <110> APPLICANT: Satoshi Harashima  
 4 Yoshinobu Kaneko  
 5 Minetaka Sugiyama  
 W--> 6 <120> TITLE OF INVENTION: Method for modifying chromosomes  
 W--> 7 <130> FILE REFERENCE: NANJ-0009-1  
 C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/659,326  
 C--> 8 <141> CURRENT FILING DATE: 2003-09-11  
 8 <150> PRIOR APPLICATION NUMBER: Japanese Patent Application No. 2002-339259  
 W--> 9 <151> PRIOR FILING DATE: November 22, 2002  
 W--> 10 <160> NUMBER OF SEQ ID: 20

## ERRORED SEQUENCES

W--> 11 <210> SEQ ID NO: 1  
 12 <211> LENGTH: 29  
 13 <212> TYPE: DNA  
 14 <213> ORGANISM: Artificial Sequence

W--&gt; 15 &lt;220&gt; FEATURE:

W--&gt; 15 &lt;223&gt; OTHER INFORMATION:

W--&gt; 15 &lt;400&gt; SEQUENCE: 1

E--&gt; 16 ctctctagat aacaccgatc agatgcaca 29

17 29

18 &lt;210&gt; SEQ ID NO: 2

19 &lt;211&gt; LENGTH: 29

20 &lt;212&gt; TYPE: DNA

21 &lt;213&gt; ORGANISM: Artificial Sequence

W--&gt; 22 &lt;220&gt; FEATURE:

W--&gt; 22 &lt;223&gt; OTHER INFORMATION:

W--&gt; 22 &lt;400&gt; SEQUENCE: 2

E--&gt; 23 ctccctcgaga aacttgctct gctaactca 29

24 29

25 &lt;210&gt; SEQ ID NO: 3

26 &lt;211&gt; LENGTH: 29

27 &lt;212&gt; TYPE: DNA

28 &lt;213&gt; ORGANISM: Artificial Sequence

W--&gt; 29 &lt;220&gt; FEATURE:

W--&gt; 29 &lt;223&gt; OTHER INFORMATION:

W--&gt; 29 &lt;400&gt; SEQUENCE: 3

E--&gt; 30 ctcgaaattcg gccattctca tgaagaata 29

31 29

32 &lt;210&gt; SEQ ID NO: 4

33 &lt;211&gt; LENGTH: 29

**Does Not Comply  
Corrected Diskette Needed**

→ see item 11 on error summary report.

29 → see item 1  
on error  
summary sheet

## RAW SEQUENCE LISTING

DATE: 09/22/2003

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Input Set : A:\NANJ-0009-1 Sequence Listing.asc

Output Set: N:\CRF4\09222003\J659326.raw

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34 <212> TYPE: DNA
35 <213> ORGANISM: Artificial Sequence
W--> 36 <220> FEATURE:
W--> 36 <223> OTHER INFORMATION:
W--> 36 <400> SEQUENCE: 4
E--> 37 ctctgaattct ctaagaggtg atacttatt 29
38 29
39 <210> SEQ ID NO: 5
40 <211> LENGTH: 99
41 <212> TYPE: DNA
42 <213> ORGANISM: Artificial Sequence
W--> 43 <220> FEATURE:
W--> 43 <223> OTHER INFORMATION:
W--> 43 <400> SEQUENCE: 5
E--> 44 gaatgctatg ttgtgggttag cgacctgccc cttgccaaat
45 ctatatcacc acttccttag 60
E--> 46 catgtaatca tttacttaaa ggaaacagct atgaccatg
47 99
48 <210> SEQ ID NO: 6
49 <211> LENGTH: 56
50 <212> TYPE: DNA
51 <213> ORGANISM: Artificial Sequence
W--> 52 <220> FEATURE:
W--> 52 <223> OTHER INFORMATION:
W--> 52 <400> SEQUENCE: 6
E--> 53 ccccaacccc aaccccaacc ccaaccccaa ccccaatcga
54 ggtcgacggt atcgat 56
55 <210> SEQ ID NO: 7
56 <211> LENGTH: 99
57 <212> TYPE: DNA
58 <213> ORGANISM: Artificial Sequence
W--> 59 <220> FEATURE:
W--> 59 <223> OTHER INFORMATION:
W--> 59 <400> SEQUENCE: 7
E--> 60 gttgaaaagg aaatcaacgt tacaaagtgc agttttttgt
61 attattttcc tattatcctc 60
E--> 62 ttcttttcct ttgtttcagg ggaaacagct atgaccatg
63 99
64 <210> SEQ ID NO: 8
65 <211> LENGTH: 99
66 <212> TYPE: DNA
67 <213> ORGANISM: Artificial Sequence
W--> 68 <220> FEATURE:
W--> 68 <223> OTHER INFORMATION:
W--> 68 <400> SEQUENCE: 8
E--> 69 tttaagtaaa tgattacatg ctaaggaagt ggtgaataag
70 atttggaag gggcaggtcg 60
E--> 71 ctaaccacaa catagcattc ggaaacagct atgaccatg
72 99
```

Same errors

## RAW SEQUENCE LISTING

DATE: 09/22/2003

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Input Set : A:\NANJ-0009-1 Sequence Listing.asc

Output Set: N:\CRF4\09222003\J659326.raw

```
73 <210> SEQ ID NO: 9
74 <211> LENGTH: 99
75 <212> TYPE: DNA
76 <213> ORGANISM: Artificial Sequence
W--> 77 <220> FEATURE:
W--> 77 <223> OTHER INFORMATION:
W--> 77 <400> SEQUENCE: 9
E--> 78 cctgaaacaa aggaaaagaa gaggataata ggaaaataat
79 acaaaaaaact gcactttgta 60
E--> 80 acgttgattt ccttttcaac ggaaacagct atgaccatg
81 99
82 <210> SEQ ID NO: 10
83 <211> LENGTH: 60
84 <212> TYPE: DNA
85 <213> ORGANISM: Artificial Sequence
W--> 86 <220> FEATURE:
W--> 86 <223> OTHER INFORMATION:
W--> 86 <400> SEQUENCE: 10
E--> 87 caagaaatat cttgaccgca gtgaactgtg ggaataactca
88 ggtatacagc tatgaccatg 60
89 <210> SEQ ID NO: 11
90 <211> LENGTH: 60
91 <212> TYPE: DNA
92 <213> ORGANISM: Artificial Sequence
W--> 93 <220> FEATURE:
W--> 93 <223> OTHER INFORMATION:
W--> 93 <400> SEQUENCE: 11
E--> 94 gaaaaaataa tggttgctaa gagattcgaa ctcttgcac
95 ttacgacagc tatgaccatg 60
96 <210> SEQ ID NO: 12
97 <211> LENGTH: 19
98 <212> TYPE: DNA
99 <213> ORGANISM: Artificial Sequence
W--> 100 <220> FEATURE:
W--> 100 <223> OTHER INFORMATION:
W--> 100 <400> SEQUENCE: 12
E--> 101 ctcgtcgacg gccattctca tgaagaata
E--> 102 19
103 <210> SEQ ID NO: 13
104 <211> LENGTH: 19
105 <212> TYPE: DNA
106 <213> ORGANISM: Artificial Sequence
W--> 107 <220> FEATURE:
W--> 107 <223> OTHER INFORMATION:
W--> 107 <400> SEQUENCE: 13
E--> 108 ctcctcgagt ctaagagggtg atacttatt
E--> 109 19
110 <210> SEQ ID NO: 14
111 <211> LENGTH: 99
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Same errors

## RAW SEQUENCE LISTING

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PATENT APPLICATION: US/10/659,326

TIME: 13:13:53

Input Set : A:\NANJ-0009-1 Sequence Listing.asc

Output Set: N:\CRF4\09222003\J659326.raw

```

112 <212> TYPE: DNA
113 <213> ORGANISM: Artificial Sequence
W--> 114 <220> FEATURE:
W--> 114 <223> OTHER INFORMATION:
W--> 114 <400> SEQUENCE: 14
E--> 115 ggtcttcacac ctccatttgg tcaatgcggc caacaatacg
116 gatttcctcc tcattggagc 60
E--> 117 gcagagaccc taacaacaca cttcgtacgc tgcaggctcg
118 99
119 <210> SEQ ID NO: 15
120 <211> LENGTH: 99
121 <212> TYPE: DNA
122 <213> ORGANISM: Artificial Sequence
W--> 123 <220> FEATURE:
W--> 123 <223> OTHER INFORMATION:
W--> 123 <400> SEQUENCE: 15
E--> 124 tgtgtggtca tgttcagcgt gagcaaaatc agtcggaaag
125 tgaacgagaa ttggaatgtg 60
E--> 126 gaagacggac atatcactga cttcgtacgc tgcaggctcg
127 99
128 <210> SEQ ID NO: 16
129 <211> LENGTH: 99
130 <212> TYPE: DNA
131 <213> ORGANISM: Artificial Sequence
W--> 132 <220> FEATURE:
W--> 132 <223> OTHER INFORMATION:
W--> 132 <400> SEQUENCE: 16
E--> 133 ttataatgag caagtogata caaggactgc ccataaagtg
134 ggaggagtac gccgctgatg 60
E--> 135 aagtgggttt gctgggtacct cttcgtacgc tgcaggctcg
136 99
137 <210> SEQ ID NO: 17
138 <211> LENGTH: 99
139 <212> TYPE: DNA
140 <213> ORGANISM: Artificial Sequence
W--> 141 <220> FEATURE:
W--> 141 <223> OTHER INFORMATION:
W--> 141 <400> SEQUENCE: 17
E--> 142 tatatgattt tgtgttcggt tttcgttctg cgaaaggcat
143 ccccaatggc ttgtttcatt 60
E--> 144 gatccatcag tgtggctcgt cttcgtacgc tgcaggctcg
145 99
146 <210> SEQ ID NO: 18
147 <211> LENGTH: 99
148 <212> TYPE: DNA
149 <213> ORGANISM: Artificial Sequence
W--> 150 <220> FEATURE:
W--> 150 <223> OTHER INFORMATION:
W--> 150 <400> SEQUENCE: 18

```

Same errors

## RAW SEQUENCE LISTING

DATE: 09/22/2003

PATENT APPLICATION: US/10/659,326

TIME: 13:13:53

Input Set : A:\NANJ-0009-1 Sequence Listing.asc

Output Set: N:\CRF4\09222003\J659326.raw

E--> 151 gaccagtga gagggaattga ataagtagaa cttgggcaat  
152 atttataacg gcaatgataa 60  
E--> 153 tgataatcaa tatagataac cttcgtacgc tgcaggtcg  
154 99  
155 <210> SEQ ID NO: 19  
156 <211> LENGTH: 99  
157 <212> TYPE: DNA  
158 <213> ORGANISM: Artificial Sequence  
W--> 159 <220> FEATURE:  
W--> 159 <223> OTHER INFORMATION:  
W--> 159 <400> SEQUENCE: 19  
E--> 160 acgaagactt tgaactatatt gagagccaga gaatggagaa  
161 acatgtctac cgtcaattcc 60  
E--> 162 accgaatcaa ggttgacttg cttcgtacgc tgcaggtcg  
163 99  
164 <210> SEQ ID NO: 20  
165 <211> LENGTH: 56  
166 <212> TYPE: DNA  
167 <213> ORGANISM: Artificial Sequence  
W--> 168 <220> FEATURE:  
W--> 168 <223> OTHER INFORMATION:  
W--> 168 <400> SEQUENCE: 20  
E--> 169 ccccaacccc aaccccaacc ccaaccccaa ccccaaaggc  
170 cactagtgga tctgat 56

*Same errors*

RAW SEQUENCE LISTING ERROR SUMMARY  
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DATE: 09/22/2003  
TIME: 13:13:54

Input Set : A:\NANJ-0009-1 Sequence Listing.asc  
Output Set: N:\CRF4\09222003\J659326.raw

Use of <220> Feature (NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20



## VERIFICATION SUMMARY

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TIME: 13:13:54

Input Set : A:\NANJ-0009-1 Sequence Listing.asc

Output Set: N:\CRF4\09222003\J659326.raw

L:6 M:283 W: Missing Blank Line separator, <120> field identifier  
L:7 M:283 W: Missing Blank Line separator, <130> field identifier  
L:8 M:270 C: Current Application Number differs, Replaced Current Application No  
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:9 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:10 M:283 W: Missing Blank Line separator, <160> field identifier  
L:11 M:283 W: Missing Blank Line separator, <210> field identifier  
L:15 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:1, <213>  
ORGANISM:Artificial Sequence  
L:15 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:1, <213>  
ORGANISM:Artificial Sequence  
L:15 M:283 W: Missing Blank Line separator, <400> field identifier  
L:15 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:15  
L:16 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:1  
L:22 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:2, <213>  
ORGANISM:Artificial Sequence  
L:22 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>  
ORGANISM:Artificial Sequence  
L:22 M:283 W: Missing Blank Line separator, <400> field identifier  
L:22 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:22  
L:23 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:2  
L:29 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:3, <213>  
ORGANISM:Artificial Sequence  
L:29 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:3, <213>  
ORGANISM:Artificial Sequence  
L:29 M:283 W: Missing Blank Line separator, <400> field identifier  
L:29 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:29  
L:30 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:3  
L:36 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:4, <213>  
ORGANISM:Artificial Sequence  
L:36 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>  
ORGANISM:Artificial Sequence  
L:36 M:283 W: Missing Blank Line separator, <400> field identifier  
L:36 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:36  
L:37 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:4  
L:43 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:5, <213>  
ORGANISM:Artificial Sequence  
L:43 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>  
ORGANISM:Artificial Sequence  
L:43 M:283 W: Missing Blank Line separator, <400> field identifier  
L:43 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:43  
L:44 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:40 SEQ:5  
M:254 Repeated in SeqNo=5  
L:52 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213>  
ORGANISM:Artificial Sequence  
L:52 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>  
ORGANISM:Artificial Sequence  
L:52 M:283 W: Missing Blank Line separator, <400> field identifier  
L:52 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:52  
L:53 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:40 SEQ:6  
L:59 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:7, <213>  
ORGANISM:Artificial Sequence  
L:59 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:7, <213>

ORGANISM:Artificial Sequence

L:59 M:283 W: Missing Blank Line separator, <400> field identifier

L:59 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:59

L:60 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:40 SEQ:7

M:254 Repeated in SeqNo=7

L:68 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>

ORGANISM:Artificial Sequence

L:68 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>

ORGANISM:Artificial Sequence

L:68 M:283 W: Missing Blank Line separator, <400> field identifier

L:68 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:68

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TIME: 13:13:54

Input Set : A:\NANJ-0009-1 Sequence Listing.asc

Output Set: N:\CRF4\09222003\J659326.raw

L:69 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:40 SEQ:8  
M:254 Repeated in SeqNo=8  
L:77 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:9, <213>  
ORGANISM:Artificial Sequence  
L:77 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:9, <213>  
ORGANISM:Artificial Sequence  
L:77 M:283 W: Missing Blank Line separator, <400> field identifier  
L:77 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:77  
L:78 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:40 SEQ:9  
M:254 Repeated in SeqNo=9  
L:86 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213>  
ORGANISM:Artificial Sequence  
L:86 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>  
ORGANISM:Artificial Sequence  
L:86 M:283 W: Missing Blank Line separator, <400> field identifier  
L:86 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:86  
L:87 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:40 SEQ:10  
L:93 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:11, <213>  
ORGANISM:Artificial Sequence  
L:93 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:11, <213>  
ORGANISM:Artificial Sequence  
L:93 M:283 W: Missing Blank Line separator, <400> field identifier  
L:93 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:93  
L:94 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:40 SEQ:11  
L:100 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:12, <213>  
ORGANISM:Artificial Sequence  
L:100 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:12, <213>  
ORGANISM:Artificial Sequence  
L:100 M:283 W: Missing Blank Line separator, <400> field identifier  
L:100 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:100  
L:101 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:12  
M:254 Repeated in SeqNo=12  
L:102 M:252 E: No. of Seq. differs, <211> LENGTH:Input:19 Found:29 SEQ:12  
L:107 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:13, <213>  
ORGANISM:Artificial Sequence  
L:107 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:13, <213>  
ORGANISM:Artificial Sequence  
L:107 M:283 W: Missing Blank Line separator, <400> field identifier  
L:107 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:107  
L:108 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:13  
M:254 Repeated in SeqNo=13  
L:109 M:252 E: No. of Seq. differs, <211> LENGTH:Input:19 Found:29 SEQ:13  
L:114 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:14, <213>  
ORGANISM:Artificial Sequence  
L:114 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:14, <213>  
ORGANISM:Artificial Sequence  
L:114 M:283 W: Missing Blank Line separator, <400> field identifier  
L:114 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:114  
L:115 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:40 SEQ:14  
M:254 Repeated in SeqNo=14  
L:123 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:15, <213>  
ORGANISM:Artificial Sequence  
L:123 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:15, <213>

ORGANISM:Artificial Sequence

L:123 M:283 W: Missing Blank Line separator, <400> field identifier

L:123 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:123

L:124 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:40 SEQ:15

M:254 Repeated in SeqNo=15

L:132 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:16, <213>

ORGANISM:Artificial Sequence

L:132 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:16, <213>

ORGANISM:Artificial Sequence

L:132 M:283 W: Missing Blank Line separator, <400> field identifier

L:132 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:132

L:133 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:40 SEQ:16

**VERIFICATION SUMMARY**

DATE: 09/22/2003

PATENT APPLICATION: US/10/659,326

TIME: 13:13:54

Input Set : A:\NANJ-0009-1 Sequence Listing.asc

Output Set: N:\CRF4\09222003\J659326.raw

M:254 Repeated in SeqNo=16  
L:141 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:17, <213>  
ORGANISM:Artificial Sequence  
L:141 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:17, <213>  
ORGANISM:Artificial Sequence  
L:141 M:283 W: Missing Blank Line separator, <400> field identifier  
L:142 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:40 SEQ:17  
M:254 Repeated in SeqNo=17  
L:150 M:283 W: Missing Blank Line separator, <400> field identifier  
L:151 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:40 SEQ:18  
M:254 Repeated in SeqNo=18  
L:159 M:283 W: Missing Blank Line separator, <400> field identifier  
L:160 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:40 SEQ:19  
M:254 Repeated in SeqNo=19  
L:168 M:283 W: Missing Blank Line separator, <400> field identifier  
L:169 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:40 SEQ:20